

#34

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/057,016
Source: 1600
Date Processed by STIC: 02-23-2005

ENTERED



1600

RAW SEQUENCE LISTING

DATE: 02/23/2005

PATENT APPLICATION: US/09/057,016

TIME: 15:06:06

Input Set : N:\Crf3\RULE60\09057016.raw.txt

Output Set: N:\CRF4\02232005\I057016.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Turpen, Thomas H.

6 Reinl, Stephen

7 Grill, Laurence K.

9 (ii) TITLE OF INVENTION: Production of Peptides in Plants as

10 Viral Coat Protein Fusions

12 (iii) NUMBER OF SEQUENCES: 27

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Pennie & Edmonds

16 (B) STREET: 1155 Avenue of the Americas

17 (C) CITY: New York

18 (D) STATE: New York

19 (E) COUNTRY: USA

20 (F) ZIP: 10036

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 34 (A) APPLICATION NUMBER: US/09/057,016

C--> 35 (B) FILING DATE: 07-Apr-1998

31 (C) CLASSIFICATION: 435

33 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Halluin, Albert P.

37 (B) REGISTRATION NUMBER: 25,227

38 (C) REFERENCE/DOCKET NUMBER: 8129-087

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 415-854-3660

42 (B) TELEFAX: 415-854-3694

43 (C) TELEX: 66141 PENNIE

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 49 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: unknown

52 (D) TOPOLOGY: unknown

54 (ii) MOLECULE TYPE: DNA (genomic)

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60 GGAATTCAAG CTTAATACGA CTCATATAG TATTTTACA ACAATTACC

62 (2) INFORMATION FOR SEQ ID NO: 2:

64 (i) SEQUENCE CHARACTERISTICS:

49

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Input Set : N:\Crif3\RULE60\09057016.raw.txt

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65      (A) LENGTH: 18 base pairs
66      (B) TYPE: nucleic acid
67      (C) STRANDEDNESS: unknown
68      (D) TOPOLOGY: unknown
70      (ii) MOLECULE TYPE: DNA (genomic)
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
76 CCTTCATGTA AACCTCTC                                     18
78 (2) INFORMATION FOR SEQ ID NO: 3:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 25 base pairs
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: unknown
84          (D) TOPOLOGY: unknown
86      (ii) MOLECULE TYPE: DNA (genomic)
90      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
92 TAATCGATGA TGATTCGAG GCTAC                               25
94 (2) INFORMATION FOR SEQ ID NO: 4:
96      (i) SEQUENCE CHARACTERISTICS:
97          (A) LENGTH: 36 base pairs
98          (B) TYPE: nucleic acid
99          (C) STRANDEDNESS: unknown
100         (D) TOPOLOGY: unknown
102      (ii) MOLECULE TYPE: DNA (genomic)
106      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
108 AAAGTCTCTG TCTCCTGCAG GGAACCTAAC AGTTAC                36
110 (2) INFORMATION FOR SEQ ID NO: 5:
112      (i) SEQUENCE CHARACTERISTICS:
113          (A) LENGTH: 36 base pairs
114          (B) TYPE: nucleic acid
115          (C) STRANDEDNESS: unknown
116          (D) TOPOLOGY: unknown
118      (ii) MOLECULE TYPE: DNA (genomic)
122      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
124 ATTATGCATC TTGACTACCT AGGTTGCAGG ACCAGA                36
126 (2) INFORMATION FOR SEQ ID NO: 6:
128      (i) SEQUENCE CHARACTERISTICS:
129          (A) LENGTH: 24 base pairs
130          (B) TYPE: nucleic acid
131          (C) STRANDEDNESS: unknown
132          (D) TOPOLOGY: unknown
134      (ii) MOLECULE TYPE: DNA (genomic)
138      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
140 GGCGATCGGG CTGGTGACCG TGCA                               24
142 (2) INFORMATION FOR SEQ ID NO: 7:
144      (i) SEQUENCE CHARACTERISTICS:
145          (A) LENGTH: 24 base pairs
146          (B) TYPE: nucleic acid
147          (C) STRANDEDNESS: unknown
148          (D) TOPOLOGY: unknown

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150      (ii) MOLECULE TYPE: DNA (genomic)
154      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
156 CGGTCACCAG CCCGATCGCC TGCA                                     24
158 (2) INFORMATION FOR SEQ ID NO: 8:
160      (i) SEQUENCE CHARACTERISTICS:
161          (A) LENGTH: 45 base pairs
162          (B) TYPE: nucleic acid
163          (C) STRANDEDNESS: unknown
164          (D) TOPOLOGY: unknown
166      (ii) MOLECULE TYPE: DNA (genomic)
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
172 CTAGCAATTA CAAGGTCCAG GTGCACCTCA AGGTCCTGGA GCTCC             45
174 (2) INFORMATION FOR SEQ ID NO: 9:
176      (i) SEQUENCE CHARACTERISTICS:
177          (A) LENGTH: 45 base pairs
178          (B) TYPE: nucleic acid
179          (C) STRANDEDNESS: unknown
180          (D) TOPOLOGY: unknown
182      (ii) MOLECULE TYPE: DNA (genomic)
186      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
188 CTAGGGAGCT CCAGGACCTT GAGGTGCACC TGGACCTTGT AATTG           45
190 (2) INFORMATION FOR SEQ ID NO: 10:
192      (i) SEQUENCE CHARACTERISTICS:
193          (A) LENGTH: 35 base pairs
194          (B) TYPE: nucleic acid
195          (C) STRANDEDNESS: unknown
196          (D) TOPOLOGY: unknown
198      (ii) MOLECULE TYPE: DNA (genomic)
202      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
204 ATTATGCATC TTGACTACCT AGGTCCAAAC CAAAC                         35
206 (2) INFORMATION FOR SEQ ID NO: 11:
208      (i) SEQUENCE CHARACTERISTICS:
209          (A) LENGTH: 66 base pairs
210          (B) TYPE: nucleic acid
211          (C) STRANDEDNESS: unknown
212          (D) TOPOLOGY: unknown
214      (ii) MOLECULE TYPE: DNA (genomic)
218      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
220 GTCATATGTT CCATCTGCAG AGCAGATCTT GGAATTCGTT AAGCAAATCT CGAGTCAGTA 60
222 ACTATA                                                         66
224 (2) INFORMATION FOR SEQ ID NO: 12:
226      (i) SEQUENCE CHARACTERISTICS:
227          (A) LENGTH: 66 base pairs
228          (B) TYPE: nucleic acid
229          (C) STRANDEDNESS: unknown
230          (D) TOPOLOGY: unknown
232      (ii) MOLECULE TYPE: DNA (genomic)
236      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
238 TATAGTTACT GACTCGAGAT TTGCTTAACG AATTCCAAGA TCTGCTCTGC AGATGGAACA 60

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240 TATGAC 66
242 (2) INFORMATION FOR SEQ ID NO: 13:
244     (i) SEQUENCE CHARACTERISTICS:
245         (A) LENGTH: 33 base pairs
246         (B) TYPE: nucleic acid
247         (C) STRANDEDNESS: unknown
248         (D) TOPOLOGY: unknown
250     (ii) MOLECULE TYPE: DNA (genomic)
254     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
256 CGACCTAGGT GATGACGTCA TAGCAATTAA CGT 33
258 (2) INFORMATION FOR SEQ ID NO: 14:
260     (i) SEQUENCE CHARACTERISTICS:
261         (A) LENGTH: 33 base pairs
262         (B) TYPE: nucleic acid
263         (C) STRANDEDNESS: unknown
264         (D) TOPOLOGY: unknown
266     (ii) MOLECULE TYPE: DNA (genomic)
270     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
272 TAATTGCTAT GACGTCATCA CCTAGGTCGA CGT 33
274 (2) INFORMATION FOR SEQ ID NO: 15:
276     (i) SEQUENCE CHARACTERISTICS:
277         (A) LENGTH: 4 amino acids
278         (B) TYPE: amino acid
279         (C) STRANDEDNESS: unknown
280         (D) TOPOLOGY: unknown
282     (ii) MOLECULE TYPE: peptide
286     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
288 Ala Gly Asp Arg
289 1
291 (2) INFORMATION FOR SEQ ID NO: 16:
293     (i) SEQUENCE CHARACTERISTICS:
294         (A) LENGTH: 510 base pairs
295         (B) TYPE: nucleic acid
296         (C) STRANDEDNESS: unknown
297         (D) TOPOLOGY: unknown
299     (ii) MOLECULE TYPE: DNA (genomic)
301     (vi) ORIGINAL SOURCE:
302         (A) ORGANISM: pBGC291 Fusion
304     (ix) FEATURE:
305         (A) NAME/KEY: CDS
306         (B) LOCATION: 1..510
309     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
311 ATG TCT TAC AGT ATC ACT ACT CCA TCT CAG TTC GTG TTC TTG TCA TCA 48
312 Met Ser Tyr Ser Ile Thr Thr Pro Ser Gln Phe Val Phe Leu Ser Ser
313 1 5 10 15
315 GCG TGG GCC GAC CCA ATA GAG TTA ATT AAT TTA TGT ACT AAT GCC TTA 96
316 Ala Trp Ala Asp Pro Ile Glu Leu Ile Asn Leu Cys Thr Asn Ala Leu
317 20 25 30
319 GGA AAT CAG TTT CAA ACA CAA CAA GCT CGA ACT GTC GTT CAA AGA CAA 144

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Input Set : N:\Crif3\RULE60\09057016.raw.txt

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320 Gly Asn Gln Phe Gln Thr Gln Gln Ala Arg Thr Val Val Gln Arg Gln
321          35          40          45
323 TTC AGT GAG GTG TGG AAA CCT TCA CCA CAA GTA ACT GTT AGG TTC CCT      192
324 Phe Ser Glu Val Trp Lys Pro Ser Pro Gln Val Thr Val Arg Phe Pro
325          50          55          60
327 GCA GGC GAT CGG GCT GGT GAC CGT GCA GGA GAC AGA GAC TTT AAG GTG      240
328 Ala Gly Asp Arg Ala Gly Asp Arg Ala Gly Asp Arg Asp Phe Lys Val
329          65          70          75          80
331 TAC AGG TAC AAT GCG GTA TTA GAC CCG CTA GTC ACA GCA CTG TTA GGT      288
332 Tyr Arg Tyr Asn Ala Val Leu Asp Pro Leu Val Thr Ala Leu Leu Gly
333          85          90          95
335 GCA TTC GAC ACT AGA AAT AGA ATA ATA GAA GTT GAA AAT CAG GCG AAC      336
336 Ala Phe Asp Thr Arg Asn Arg Ile Ile Glu Val Glu Asn Gln Ala Asn
337          100          105          110
339 CCC ACG ACT GCC GAA ACG TTA GAT GCT ACT CGT AGA GTA GAC GAC GCA      384
340 Pro Thr Thr Ala Glu Thr Leu Asp Ala Thr Arg Arg Val Asp Asp Ala
341          115          120          125
343 ACG GTG GCC ATA AGG AGC GCG ATA AAT AAT TTA ATA GTA GAA TTG ATC      432
344 Thr Val Ala Ile Arg Ser Ala Ile Asn Asn Leu Ile Val Glu Leu Ile
345          130          135          140
347 AGA GGA ACC GGA TCT TAT AAT CGG AGC TCT TTC GAG AGC TCT TCT GGT      480
348 Arg Gly Thr Gly Ser Tyr Asn Arg Ser Ser Phe Glu Ser Ser Ser Gly
349          145          150          155          160
351 TTG GTT TGG ACC TCT GGT CCT GCA ACT TGA      510
352 Leu Val Trp Thr Ser Gly Pro Ala Thr
353          165
356 (2) INFORMATION FOR SEQ ID NO: 17:
358 (i) SEQUENCE CHARACTERISTICS:
359 (A) LENGTH: 169 amino acids
360 (B) TYPE: amino acid
361 (D) TOPOLOGY: linear
363 (ii) MOLECULE TYPE: protein
365 (vi) ORIGINAL SOURCE:
366 (A) ORGANISM: pBGC291 Fusion
368 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
370 Met Ser Tyr Ser Ile Thr Thr Pro Ser Gln Phe Val Phe Leu Ser Ser
371 1 5 10 15
373 Ala Trp Ala Asp Pro Ile Glu Leu Ile Asn Leu Cys Thr Asn Ala Leu
374 20 25 30
376 Gly Asn Gln Phe Gln Thr Gln Gln Ala Arg Thr Val Val Gln Arg Gln
377 35 40 45
379 Phe Ser Glu Val Trp Lys Pro Ser Pro Gln Val Thr Val Arg Phe Pro
380 50 55 60
382 Ala Gly Asp Arg Ala Gly Asp Arg Ala Gly Asp Arg Asp Phe Lys Val
383 65 70 75 80
385 Tyr Arg Tyr Asn Ala Val Leu Asp Pro Leu Val Thr Ala Leu Leu Gly
386 85 90 95
388 Ala Phe Asp Thr Arg Asn Arg Ile Ile Glu Val Glu Asn Gln Ala Asn
389 100 105 110

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/057,016

DATE: 02/23/2005

TIME: 15:06:07

Input Set : N:\Crf3\RULE60\09057016.raw.txt

Output Set: N:\CRF4\02232005\I057016.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vi)
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:592 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21